GGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT M.avium GGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT M.paratuberc. GGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT M.paratuberc. GGGGAACCCAGCACGAGTGATGTCGTGTTACCCGTATCT M.phlei GGGGAACCCAACGAGTGATGTCGTGTTACCCGTATCT M.leprae GGGGAAACCCAGCACGAGTAATGTCGTGTTACCCGTATCT M.gastri GGGGAAACCCAGCACGAGTGATGTCGTGTTACCCGCATCT M.kansasii GGGGAAACCCAGCACGAGTGATGTCGTGTTACCCGCATCT M.smegmatis	422 422 507 432 207 150	GGGGAACCCAGCA GGGGGAACCCGGCA GGGGAAACCCAACA GGGGAAACCCAGCA	CGAGTGATGT CGAGTGATGT CGAGTGATGT CGAGTGATGT CGAGTAATGT	CGTGTTACCCC CGTGTTACCCC CGTGTTACCCC CGTGTTACCCC CGTGTTACCCC	AACGCT M.phlei GTATCT M.leprae GTATCT M.gastri GCATCT M.kansasii
--	--	---	--	---	--

210 220 230 240 1172 CATCTCAGTACCCGTAGGAGGAGAAACAATTGTGATTCC M.tuberculosis 501 CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.avium 501 CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.paratuberc. 586 CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.phlei 511 CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.leprae 286 CATCTCAGTACCCGTAGGAGAAAACAAAAGTGATTCC M.gastri 229 CATCTCAGTACCCGTAGGAGAAAAAAAAAGTGATTCC M.kansasii 2667 CATCTCAGTFCCCGTAGGAAAAAAAAAAAAAAGTGATTCC M.smegmatis					-	
CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.paratuberc. CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.paratuberc. CATCTCAGTACCCGTAGAAGAAAACAATTGTGATTCC M.phlei CATCTCAGTACCCGTAGGAGAAAACAATTGTGATTCC M.leprae CATCTCAGTACCCGTAGGAGAAAACAAAAGTGATTCC M.gastri CATCTCAGTACCCGTAGGAGAAAACAAAAGTGATTCC M.kansasii		210	220			
	501 501 586 511 286 229	CATCTCAGTACCCGTCATCTCAGTACCCGTCATCTCAGTACCCGTCATCTCAGTACCCGTCATCTCAGTACCCGTCATCTCAGTACCCGTCATCTCAGTACCCGTCATCTCAGTACCCGTCATCTCAGTACCCGT	Paggagaaa Paggagaaaa Paggagaaaa Paggagaaa Paggagaaaa	AAACAATTGTG AAACAATTGTG AAACAATTGTG AAACAATTGTG AAACAATTGTG AAACAATTGTG	CATTCC CATTCC CATTCC CATTCC CATTCC	M.paratuberc. M.phlei M.leprae M.gastri M.kansasii

	330	340	350	360
			TA CCCGGCTGI	GA-GG M.tuberculosis
1289	TGTGGGAG-GATATC	TCTCAGCGC	ACCCGGCTOZ	AGA-GG M.tuberculosis
629				
404	IGIGGGAIGGAI	TTCTCAGCTC	TACCCGGCTG	AGG-GG M.kansasii
347	TGTGGGAITOGATAG		ma come come	GAGGG M.smegmatis
2785	TGTGGGACCTATQT	ILCHCFOCTIC	TACCERGOTO	GAGGG M.smegmatis

Figure 1A

-	370	380	390	400	tuberculosis
656 656 742 668	AGTCAGAAAGT AGTCAGAAAGT AGTCAGAAAGT IAGTCAGAAAG IAGTCAGAAAG CAGTCAGAAAG CAGTCAGAAAG CAGTCAGAAAG	ATCGTGGTTA ATTGGTGGTTA CATGGTGGTTA ATTGGTGGTTA TGTCGTGGTTA	DOSTRARDOS DOSTRARDES DOSTRARDOS DOSTRARDOS ROSTRARDOS DOSTRARDOS	CTGGGAT M CTGGGAT M CTGGGAT M	.phlei .leprae .gastri
	450	460	470	480	w tuberculosis
1406 735 735 820 747 522 465 2902	CGGCACCTGCC CGGCACCTGCC TGGCACCTGCC CGGCACCTGCC	CTTATATCAAC TGTCACAGG CTTGTATCAAT	ACCCGAGTAGO TCCCGAGTAGO TCCCGAGTAGO TCCCGAGTAGO	CAGCGGGCC CAGCGGGCC CAGCGGGCC	M.phlei M.leprae M.gastri
	49	50	0 510		
1446 775 775 857 787 562 505	CGTGGAATC CGTGGAATC CGTGGAATC CGTGGAATC CGTGGAATC	GCTGTGAATC GCTGTGAATC GCTGTGAATC GCTGTGAATC IGCTGTGAATC	GECCGGGACCA TGCCGGGACCA TGCCGGGACCA TGCCGGGACCA TGCCGGGACCA	ACCCGGTAAG ACCCGGTAAG ACCCGGTAAG ACCCGGTAAG	M.phlei M.leprae

Figure 1B

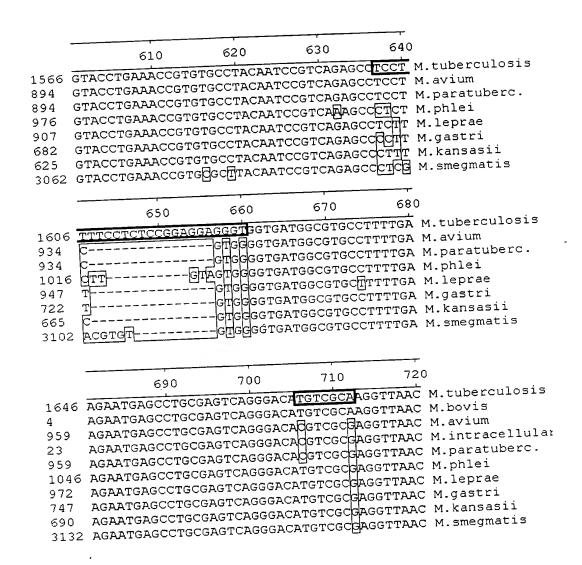


Figure 1C

				
	770	780	790	800
OF CENCECA	CACGCGCAT	ACGCGCGTGT	gaa tagtgg	CGTGT M.tuberculosis
CGACCCA	CACGUGUAL	ACGCCCC1	A GTGG	CGTGT M.avium
39 CG	Calidodolit	rggggngt rggggngt	AGTGG	CGTGT M.intracellular
3 CG	CATCCCTTI	TGGGGTGT	AGTGG	CGTGT M.paratuberc.
39 CG 26 CGTATCK	TACCTGITTG	GGGTTGGTGT	AGTGG	ПGTGT M.phlei CGTGT M.leprae
2 CGTAT-	-CACGIIGITGF	GCGNGNGT	AGTGG	CGTGT M.gastri
7 CGTAT-	-CACGCGTA -CGCGCGCGA	GCGIIGIIGT	א כידיכי	CCTGT M.kansasil
0 CGTAT- 12 CGTAT-	-CCACACAA	AGTGTGTGG	rgragtg	GIGTGT M.smegmatis
12 00[1711]				
		- -		
				1000
	970	980	990	
26 ATTTAG	GTGCAGCGT	TGCGTGGTTC	ACCIGICGAG	GTAGAG M.tuberculosis GTAGAG M.avium
228 ATTTA	GTGCAGCG1	1000100110	T CONCEGAG	GTAGAG M.paratuberc.
28 ATTTA	GTGCAGCG1 CCTGCAGCG1	GCATGITTC	TTATCGGAG	GTAGAG M.phlei GGTAGAG M.leprae
22 ATTTA	GTGCAGCGT	TGCGTGGTTC	CACCACGGAC	GGTAGAG M.leprae GGTAGAG M.gastri
ነ13 አጥጥጥል	GTGCAGCG	1.190010 1 -1.		agrancia M kansasil
62 ATTTA	GGTGCAGCG'	r-GCGTGHTT r-GCATGHTT	TTGCCGGA	GGTAGAG M.smegmatis
108 ATTTA	GGTGCAGCG	- FO OFF - FP		
		-		
	1050	1060	1070	1080
OOS CAGCO	CAAACTCCGA	ATGCCG-TGG	TG-TA-AA	CGTGGCA M.tuberculosi
ISO7 CAGC	CAAACTCCGA	MIGCOC 10	ع م مام م	corceca M.paratuberc.
1307 CAGC	CAAACTCCGA	AATGCCG-1GC	- m-7000	EMGTGGCA M.phlei
1401 CAGC	CAAACTCCG/ CAAACTCCG/	AATGCCG-TG	TIT-TAPAA	GCGTGGCA M.leprae GCGTGGCA M.gastri
1323 CAGC	CAAACTCCG	AATGCCG-TG	STG-TATA-	GCGTGGCA M.gastri GCGTGGCA M.kansasii
1041 CAGC	CAAACTCCG:	AATGCCG-TG	GTG-TAUAT	GCGTGGCA M.kansasii GTGGGGAA M.smegmatis
3486 CAGC	CAAACTCCG	AATGCCGGTA	VOOD ALTON	-0 -0 -0

Figure 1D

1385 1385 1479 1401	ACAGCCCAGATCGCCACAGCCCAGATCGCCAGATCGCCAGATCGCCAGATCGCACAGATCGCACAGATCGCACAGATCGCACAGATCGCACAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCCCAGATCGCACAGCACAGCCCAGATCGCACAGCACAGCACAGCACAGCACAGATCGCACACAGCACAGCA	CGGCTAAGGCC CGGCTAAGGCC CGGCTAAGGCC CGGCTAAGGCC	CCTAAGCGT CCTAAGCGT CCTAAGCGT CCTAAGCGT	

					 -
	129			1310	1320 GT- M.tuberculosis
2241 1544 1544 1638 1560 1334 1277 3726	CTCAAGCACAC CTCAAGCACAC CTCAAGCACAC CTCAAGCACAC CTCAAGCACAC CTCAAGCACAC	CCGCCGAAG CCGCCGAAG CCGCCGAAG CCGCCGAAG	CCGCGGCAC CCGCGGCAC CCGCGGCAC CCGCGACA CCGCGACA	CATICATOTTATCAGCOT CATICACCTTACCGC	TA M.avium TA M.paratuberc. TTG M.phlei TOTA M.leprae C-A M.gastri C-A M.kansasii
	133		340	1350	1360
2280 1583 1583 1676 1600 136 1310 376	GGGTGGATGT GGTGGATGT GGTGGTGT GGGTGGATGT GGGTGGATGT GGGTGGATGT GGGTGGATGT GGGTGGATGT GGGTGGATGT GGGTGGATGT	GGGTAGGGC GGGTAGGGC GGGTAGGGC GGGTAGGGC TGGGTAGGGC	AGCGTCCC AGCGTCCC AGCGTCCC AGCGTCCCC AGCGTCCCC	CATTCAGC	GAAG M.paratuberc. GAAG M.phlei GAAG M.leprae GAAG M.gastri CGAAG M.kansasii

Figure 1E

				
	1370	1380	1390	1400
1623 CT-CCG 1623 CT-CCG 1716 CCGCCG 1640 CCTCCG 1402 CCGCCG	ggtgaccgg ggtga∏cgg Agtga∏cgg ggtAaccgg ggtgaccgg	TGGTGGAGGG TGGTGGAGGG TGGTGGAGGG TGGTGGAGGA	TGGGGGAGT TGTGGGGAGT TGGGGGAGT TGGGGGAGT	GAGAAT M.tuberculosis GAGAAT M.avium GAGAAT M.paratuberc. GAGAAT M.phlei GAGAAT M.leprae GAGAAT M.gastri GAGAAT M.kansasii GAGAAT M.smegmatis
	1410	1420	1430	1440
1662 GCAGGG 1662 GCAGGG 1756 GCAGGG 1680 GCAGGG 1442 GCAGG	CATGAGTAG CATGAGTAG CATGAGTAG CATGAGTAG CATGAGTAG	CGATAAGGCA CGATAAGGCA CGATAAGGCA CGATAAGGCA	AGTGAGAAC AGTGAGAAC AGTGAGAAC AGTGAGAAC	CTTGCCC M.tuberculosis CTTGCCC M.avium CTTGCCC M.paratuberc. CTTTCCC M.phlei CTTGCCC M.leprae CTTGCCC M.gastri CTTGCCC M.kansasii CTTCCCC M.smegmatis
		-		
	1570	1580	1590	1600
1821 CGTCG 1821 CGTCG 1915 CGTCG 1840 CGCCG 1602 CGCC	COTGANGAA COTGANGAA COTGANGAA COTGANGAA COTGANGAA	rca-geggta rca-geggta re <u>reatte</u> tg rca-geggta rca-geggta	TAACCACC CTAACCACCC CTACCACCCC	CAAAACCG M.tuberculosis CAAAACCG M.avium CAAAACCG M.paratuberc. CAAAACCI M.phlei CAAAACCG M.leprae CAAAACCG M.gastri CAAAACCG M.kansasii CAAAACCA M.smegmatis

Figure 1F

				
-	1610	1620	1630	1640
1860 G 1860 G 1955 G 1879 G	BAT-CGACCAI-TCCCC BAT-CGACCAI-TCCCC BCC-CGATC-ATCC- BAT-CGACCAITATCCCC BAT-CGATCAC-TCCCC	TTCGGGGGC TTCGGGGGC CTTCGGGGGC	-GTGGGGATT- -GTGACGGTT TATGGAGGTT- -GTGGAGGTC	G-GG M.phlei -GGG M.leprae -TGG M.gastri
	1650	1660	1670	1680
1896 1896 1986 1917 1677	GGCTGCGTGGGAACTT GGCTGCGTGGGACCTT GGCTGCGTGGGACCTT GGCTGCGTGGGAACTT GGCTGCGTGGGAACTT GGCTGCGTGGAGCCTT	CGCTGGTAG G-GTGGGTAG FCGTTGGTAG	TAGTCAAGCAATAGTCAAGCGAATAGTCAAGCGAAGCGA	TGGG M.phlei
	1690	1700	1710	1720
2634 1936 1936 2025 1957 1717 1660	GTGACGCAGGAAGG GTGACGCAGGAAGG GTGACGCAGGAAGG GTGACGCAGGAAGG GTGACGCAGGAAGG GTGACGCAGGAAGG	CAGCCGTAC CAGCCGTAC CTAGCCGTAC CTAGCCGTAC	CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT CAGTCAGTGGT	гдапа- M.phlei гарпа- M.leprae

Figure 1G

```
1760
                                                     1750
                    1730
                                     1740
2672 -CTGGGGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
2672 -CTGGGGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
1974 -CTGGGGCAAGCCGGTAG-AGAGCGATAGGCAAATCCGT M.avium
1974 -CTGGGGCAAGCCGTAG-AGAGCGATAGGCAAATCCGT M.paratuberc.
2063 -CGGGGTAAACCTGTAGGGCGAGTAGGCAAATCCGT M.phlei
1995 -CTGGAGCAAGCCGTAGGGAGAGCGATAGGCAAATCCGT M.leprae
1755 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.gastri
1698 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.kansasii
1698 -CCGGGGTAAGCCAGTAGGGAGAGCGATAGGTAAATCCGT M.smegmatis
                                                                       2000
                                                       1990
                                      1980
                      1970
 2908 AGGGGGACCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.tuberculosis
 2208 AGGGGGCCGGAATACCGTGAACACCCTTGCGGTGGAGC M.avium
2208 AGGGGGCCGGAATACCGTGAACACCCTTGCGGTGGAGC M.paratuberc.
2298 AGGGGGACCCACGTACCGTGAGGGCTCTTGCGGTGGGAGC M.phlei
  2231 AGGGGGGCCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.leprae
  1934 AGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.kansasii
  4385 AGGGGGACCCACATEGCGTGTAAGCCTTTACGGCCCAAGC M.smegmatis
                                                                       2440
                                                       2430
                                       2420
                       2410
   3345 ACCTCGACGCCAGTTGGGGGCGGGGTCGTTGTTGAAATACC M.tuberculosis
           ACCTCGACGCCAGTTGGGGCGGAGTCGTTGTTGAAATACC M.bovis
   2645 GCACAGACGCCAGTTTGTTGTGGAGTCGTTGTTGAAATACC M.avium
           ATACAGACGCCAGTTTGTATGGAGTCGTTGTTGAAATACC M.intracellulare
   2645 GCACAGACGCCAGTTTGTGTGGAGTCGTTGTTGAAATACC M.paratuberc.
2737 GCTCGGACGCCAGTTCGGGTGGAGTCGTTGTTGAAATACC M.phlei
    2668 ACHTCGACGCHAGTTGGGGHGGAGTCGTTGTTGAAATACC M.leprae
                                                                             M.gastri
    2372 ACCTCAACGCCAGTTGGGGGTGGAGTCGTTGTTGAAATACC M.kansasii
    4822 GCTCACACGCCAGTGTGGGGGGGGGGGTCGTTGTTGAAATACC M.smegmatis
```

Figure 1H

					
	24	150	2460	2470	2480
1 AC 35 AC 35 AC 77 AC 08 AC	CTCTGATC CTCTGATC CTCTGATC CTCTGATC CTCTGATC	ETATTGG ETATTGG ETATTGG ETATTGG ETATTGA	ACACCTAACG ACACCTAACG ACACCTAACG GCOTCTAACC ACATCTAACC	TCGAACCCT TCGAACCCT TCGAACCCT TCGGACCGT TCGAACCGT	GAATC M.tuberculosis GAATC M.bovis TATC M.avium TATC M.intracellulare TATC M.paratuberc. GATC M.phlei ATATC M.leprae M.gastri GAATC M.kansasii
_		 2490	2500	2510	2520
54 (724 (72 (724 (817 748	gggtttag gggttdac gggttdac gggttdac dggtttac dggtttac	GGACAGT GGACAGT GGACAGT GGACAGT GGGACAGT	GCCTGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TAGTTTAAC TAGTTTAAC TAGTTTAAC TAGTTTAAC	TGGGGC M.tuberculosis TGGGGC M.bovis TGGGGC M.avium TGGGGC M.intracellular TGGGGC M.paratuberc. TGGGGC M.phlei TGGGGC M.leprae M.gastri TGGGGC M.kansasii TGGGGC M.smegmatis
			-		
		2930	2940	2950	2960
3163 3163 3256 3187 1910	AGTACGA AGTACGA AGTACGA	AGAGGACC AGAGGACC AGAGGACC	CGGGACGGAC CGGGACGGAC	GAACCTCTG GAACCTCTG GAACCTCTG	GTGCACCA M.tuberculos: GTATACCA M.avium GTATACCA M.paratuberc GTATACCA M.phlei GTATACCA M.leprae M.gastri GTGCACCA M.kansasii GTATACCA M.smegmatis

Figure 11

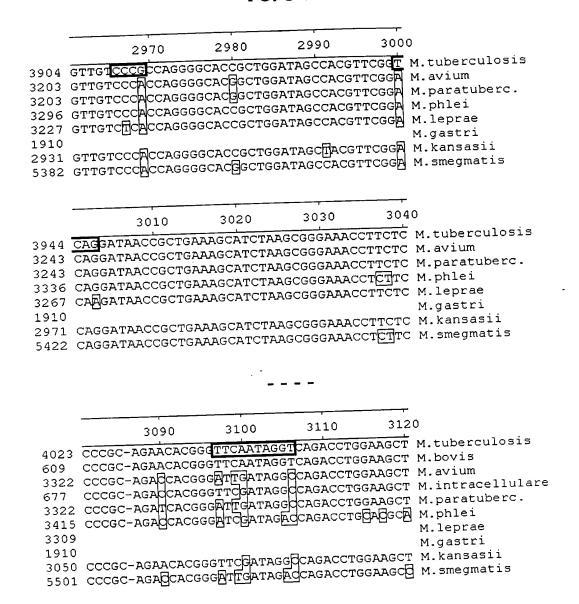
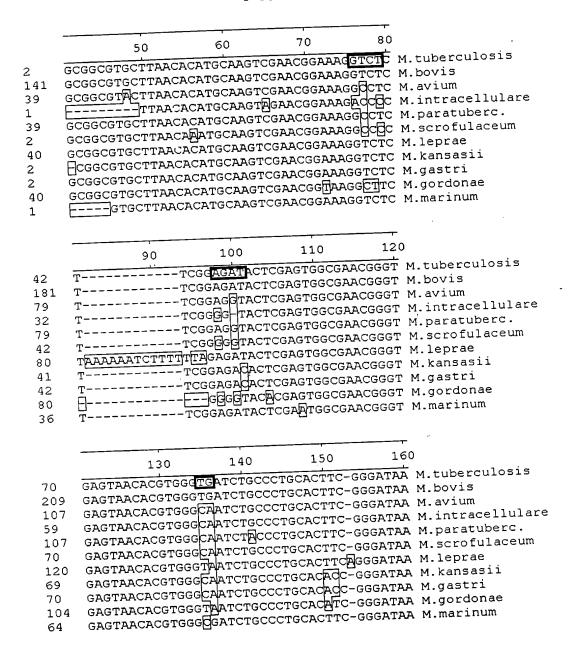
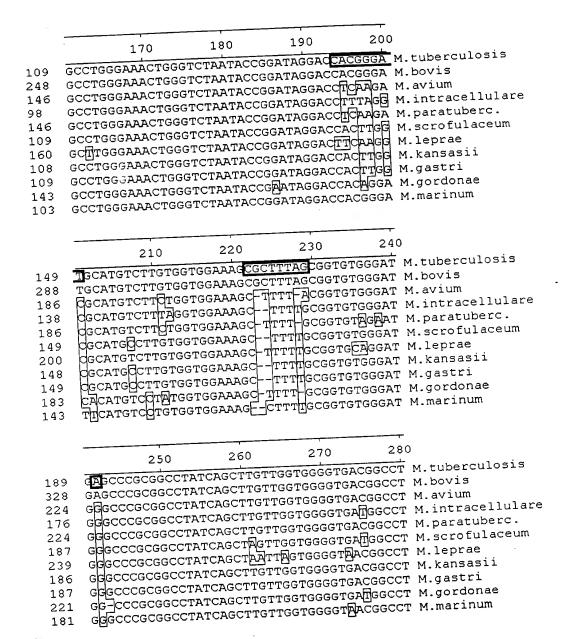


Figure 1J





	450	460	470	480
389 528 424 376	AAACCTCTTTCACC AAACCTCTTTCACC AAACCTCTTTCACC AAACCTCTTTCACC	ATCGACGAAG ATCGACGAAG ATCGACGAAG	GTCCGGGTTT GTCCGGGTTTT	TCTCGG M.intracellulare
424 387 439	AAACCTCTTTCACC	:ATCGACGAAG :ATCGACGAAG	GTCTGGGAAT GTCTGGGTTC	TCTCGG M.leprae
386 387 420 381	AAACCTCTTTCACC	CATCGACGAAG	cacceeeaan 'cacceeeaan	CTCTCGG M.gastri TCTCGG M.gordonae TCTCGG M.marinum

	1130	1140	1150	116	-
1208 1104 1056 1098 1064	TCTCATGTTGCCAGC	CGTAATGG ACGTAATGC GGGTAATGC GGGTAATGC GGGTAATGC ACGTAATGC GGGTAATGC	TEGGGACTCGTO TEGGGGACTCGTO GGGGGACTCGTO GGGGACTCGTO GGGGACTCGTO TGGGGACTCGTO GGGGGACTCGTO GGGGGACTCGTO	GAGAG GAGAG GAGAG GAGAG GAGAG GAGAG GAGAG	M.tuberculosis M.bovis M.avium M.intracellulare M.paratuberc. M.scrofulaceum M.leprae M.kansasii M.gastri M.gordonae
1061	TOTCATGITGCCAGO	7001.2.			

	1250	1260	1270	1280	
1328 1224 1176 1218 1184	CAATGGCCGGTACAA	AAGGGCTGCGA AAGGGCTGCGA AAGGGCTGCGA AAGGGCTGCGA AAGGGCTGCGA AAGGGCTGCGA AAGGGCTGCGA AAGGGCTGCGA	TGCCGCGAGG TGCCGTAAGG TGCCGCAAGG TGCCGCAAGG TGCCGCAAGG TGCCGCAAGG TGCCGCAAGG TGCCGCAAGG TGCCGCAAGG TGCCGCAAGG TGCCGCGAGG TGCCGCGAGG	ETTAAG METTAAG	M.avium M.intracellulare M.paratuberc M.scrofulaceum M.leprae M.kansasii M.gastri M.gordonae
1181	CAATGGCCGGTACA	<u> </u>			

	1290	1300	1310	1320	, muhamgulogis
1368 CGAATCC' 1264 CCAATCC' 1216 CGAATCC' 1258 CGAATCC' 1224 CGAATCC' 1279 CGAATCC 1226 CGAATCC 1227 CGAATCC	PAAAACTTTA BAAATTTTT BAAATTTTTTTTTTTTTTTT	CGGACTCA CGGGTCTCA CGGGTCTCA CGGGTCTCA CGGGTCTCA CCGGTCTCA CCGGTCTCA	GTTCGGATTG	GGGTCT M GGGTCT M GGGTCT M GGGGTCT M	M.intracellulare M.paratuberc. M.scrofulaceum M.leprae M.kansasii M.gastri M.gordonae
	1330	1340	1350	1360	
1407 GCAACT 1304 GCAACT 1256 GCAACT 1298 GCAACT 1264 GCAACT 1319 GCAACT 1266 GCAACT 1267 GCAACT	TGACCCG CGACCCA AGACCCA CGACCCGA CGACCCG CGACCCG	TGAAGTCGG TGAAGTCGG TGAAGTCGG TGAAGTCGG TGAAGTCGG TGAAGTCGG TGAAGTCGG TGAAGTCGG TGAAGTCGG	AGTCGCTAGT AGTCGCTAGT AGTCGCTAGT AGTCGCTAGT AGTCGCTAGT AGTCGCTAGT	AATCGCA AATCGCA AATCGCA AATCGCA AATCGCA AATCGCA AATCGCA AATCGCA AATCGCA	M.intracellulare M.paratuberc. M.scrofulaceum M.leprae M.kansasii M.gastri M.gordonae

Figure 2D

128 39 41 3559 5743	TGCCGAACCCGGA	AGCTAAGCCTG AGCTAAGCCTG	cagogoda :cagogoda:	80 TGATAC M.tuberculosis TGATAC M.bovis TGATAC M.phlei TGATAC M.leprae TGATAC M.smegmatis	
168 79 81 3599 5782	TGCCCTCACCGG TGCCCATTCGGG	GTGGAAAAG GTGGAAAAG	TAGGGCACCG TAGGACACCG	120 GCCGAAC M.tuberculosis GCCGAAC M.bovis GCCGAAC M.phlei GCCGAAC M.leprae GCCGAAC M.smegmatis	ŏ

Figure 3

	90	100	110	120	
382 382 1053 467 392 167 110 2548	GGGAGCTGTCAACCG GGGAGCTGTCAACCG GGGAGCTGTCAACCG	AGCATTGAT AGCGTGGAT AGCGTGGAT AGCGTGGAT	CCGAGGATTTC CCGAGGATTTC CCGAGGATTTC CCGAGGATTTC	CCGAAT CCGAAT CCGAAT	M.tuberculosis M.phlei M.leprae M.gastri M.kansasii

	170	180	190	200	
		CCACCT	ACGCGGGGAAG	STGAAA	M.avium
462	GAATATATAGGGTGCG	-GGAGGI	T CCCCCTT	AAADTE	M.paratuberc.
462	GAATATATAGGGTGCG GAATATATAGGGTGCG GAATATATAGGGTGCG	,-GGAGG <u>T</u> /	AMOROPED PAR	31022	M tuberculosis
1133					
547	GAATATATAGGGTGCG GAATATATAGGCTTCC GAATATATAGGGTTCC	3-66556		CTCDDD	м.leprae
472					
247	GAATATATAGGGTGCC		A A CCCGGGGGA A	GTGAAA	M.kansasii
190	GAATATATAGGGTGCC GAATATATAGGCGTC	3-GGAGGP	AACOOODIAA	CTCTTT	M smeamatis
•	CARTATACCCCTC	ri-gggggg	aacgcggggaa	G.I.GAAA	M. Billegillas = 1
2628	GAATATATAGGGGA				

	250	260	270	280	
	-GTCAGTAGTGGCG	ACCENTO-CG	GAACA-GGCTA	<i>LAACCG</i>	M.avium
541·	-GTCAGTAGTGGCGA	ACCCAAC-CG	GAACA-GGCT	AAACCG	M.paratuberc.
541	-GTCAGTAGTGGCG	CO DAAGUGA	CANCA-GGCT	AAACCG	M.tuberculosis
1212	-GCAAGTAGTGGCG	AGCGAACGCG		DAACCG	M.tuberculosis M.phlei
626	-GCAAGTAGTGGCG -GTGAGTAGTGGCG	AGCGAALAGG	CAGGATGGCT.	DDDCCG	M.leprae
551	-GCAAGTAGTGGCG	AGCGAACGIG	GAAIIA10001	NAACCG	M.gastri
326	-GTCAGTAGTGGCG	AGCGAACGCG	GAACAIGGCI	777777	M kansasii
269	-gtaagtagtggcg	agcgaacgc	GAACAIIGGCI		M smeamatis
2706	-gtaagtagtggcg Ggtgagtagtggcg	AGCGAACAC	GAGGAIIGGCT	AMACEG	M. Smegmer-

Figure 4A

```
310
                                                        320
                 290
     CATG-CATGGACAACCGGGTAGGGGTTGTGTGTGCGGGGT M.avium
      CATG-CATGGACAACCGGGTAGGGGTTGTGTGTGCGGGGT M.paratuberc.
1250 CAGG-CATGGGTAACCGGGTAGGGGTTGTGTGTGCGGGGT M.tuberculosis
      CETG-CATEFGATACCCGGGTCGGGGGTTGTGTGTGCGGFGT M.phlei
664
      САСА-САТСТСТБАСТАССТАССТАССТТСТСТСТССССЕЙСТ M.leprae
590
      CAGE-CATGGGTGACCGGGTAGGGGTTGTGTGTGCGGGGT M.gastri
365
      CAGG-CATGGGTACCGGGTAGGGGTTGTGTGTGCGGGGT M. kansasii
308
2745 TATGACATGTGATACCGGGTAGGGGTTGTGTGTGCGGGGT M.smegmatis
                                                         360
                                            350
                               340
                  330
       TGTGGGATTGATATGTCTCAGGTCTACCTGGCTGAGG-GG M.avium
TGTGGGATTGTTCTCAGCTCTACCTGGCTGAGG-GG M.paratuberc.

TGTGGGAG-GATATGTCTCAGCCTCTACCTGGCTGAGG-GG M.paratuberc.

TGTGGGAG-GATATGTCTCAGCGCTCACCGGGCGATGGCAG M.tuberculosis

TGTGGGGCCTGTGTGTCTCAACCTCGCCGGCGATGGCAG M.phlei

TGTGGGATTGGTATGTCTCAACTCTACCTGGTTGAGG-GG M.leprae
       TGTGGGATGGATACGTCTCAGCTCTACCCGGCTGAGG-GG M.gastri
TGTGGGATCGATACGTCTCAGCTCTACCCGGCTGAGG-GG M.kansasii
 404
 2785 TGTGGGACCTATGTTTCHCGCCTCTACCTGGCTGHGAGGG M.smegmatis
                                                          400
                                             390
                                380
                  370
       TAGTCAGAAAGTGTCGTGGTTAGCGGAAGTGGCCTGGGAC M.avium
 656 TAGTCAGAAAGTGTCGTGGTTAGCGGAAGTGGCCTGGGAC M.paratuberc.
 1327 GAGTCAGAAAGTGTCGTGGTTAGCGGAAGTGGCCTGGGAT M.tuberculosis
        TAGTGAMAAAGCAGTGTGGTTAGGTGAAGTGGCCTGGGAT M.phlei
        TAGTCAGAAAGTGCCGTGGTTAGCGGAAATGGCCTGGGAT M.leprae
        CAGTCAGAAAGTGTCGTGGTTAACGGAAGTGGCCTGGGAT M.gastri
CAGTCAGAAAGTGTCGTGGTTAACGGAAGTGGCCTGGGAT M.kansasii
  443
  2823 CAGTGAGAAAATGTTTGTGGTTAGCGGAAATGGCTTTGGGAT M.smegmatis
```

Figure 4B

	410	420	430	440
696 G 1367 G 782 G 708 G 483 G	GNCTGCCGTAGACGG GNCTGCCGTAGTGGG GCCTGCCGTAGACGG GNCTGCCGTAGACGG	TGAGAGCCC TGAGAGCCC TGAGAGCCC TGAGAGCCC	GGTACGCGAAA GGTACGCGAAA GGTACGCGAAA GGTACGTGAAA	A-ACC M.tuberculosis A-ACA M.phlei A-GCC M.leprae
_			470	480
	450	460	470	
735 1406 820	CGGCACCTGCCTAGT NGCTGCCGCTGTCA NGGCACCTGCCTTGT CGGCACCTGCCTTGT	ATCAACACC ATCAATTCC CAGGTCC ATCAATTCC ATCAATTCC	CGAGTAGCAGC CGAGTAGCAGC CGAGTAGCAGC CGAGTAGCAGC	GGGCC M.tuberculosis GGGCC M.phlei GGGCC M.leprae
		· · -		
	570	580	590	600
855 855 1526 937 867 642 585 3022	gagggaatggtgaa gagggaatggtgaa gagggaatggtgaa gagggaatggtgaa	AAGTACCCC AAGTACCCC AAGTACCCC AAGTACCCC	ggagggagt gggagggagt gggagggagt gggaggga	GAAAGA M.tuberculosis

Figure 4C

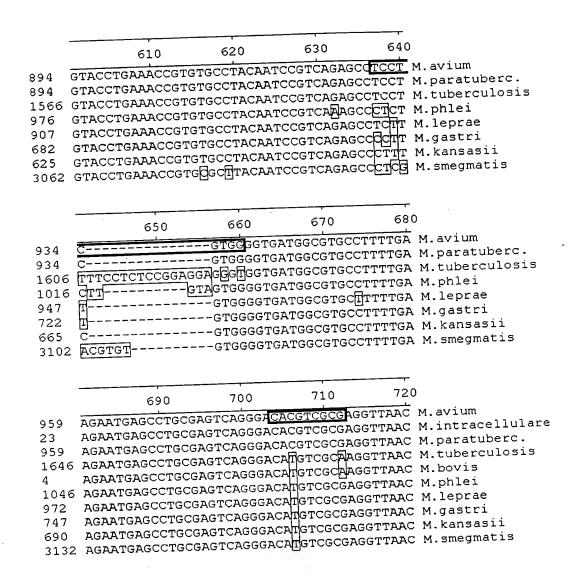


Figure 4D

					
•		770	780	790	800
1000	aden mecee	CTTTGGG	G'	TETAGTGGCGT	GT M.avium
1039	CGCATCCC CGCATCCC	CTTTGGG	G	TGTAGTGGCGT	GT M.intracellulare
1039	CGCATCCC	TTTTGGG	G	TGTAGTGGCGT	GT M.paratuberc.
			CGCGCGTGTG	AATAGTGGCGT	GT M.tuberculosis GT M.bovis
84	CGACCCAC	ACGOGCA <u>TA</u>		TGTAGTGGTGT	GT M.phlei
1126	CGTATCC	ACOTGTT CGTGTGAGCG	m	тстастссссТ	rgr M.leprae
1052 827	CGMATCAC	CGCGTAAGCG	m	TGTAGTGGCGT	rgr M.gastri
770				TGTAGTGGCGT	rgr M.kansasii
3212	CGTATCC	ACACAAGAGI	GTGTGG	TGTAGTGGE	rGT M.smegmatis
	-				
		1050	1060	1070	1080
1 207	CACCCAI	AACTCCGAAT	GCCG-TGGT	-TAAAAGCGT	GGCA M.avium GGCA M.paratuberc.
1307	CAGCCA	AACTCCGAAT	GCCG-TGGT	-TAAAAGCGT	GGCA M.paratuberc. GGCA M.tuberculosis
2005	CAGCCA	AACTCCGAAT	GCCG-TGGT	G-TAHAAGCGT	GGCA M.tuberculosis
1401	L CAGCCA	AACTCCGAA!	rgccgamaa.		GGCA M.leprae
1323	3 CAGCCA	AACTCCGAA:	recce-reeri	g-tamaFgcgt	GGCA M.gastri
1098	CAGCCA	AACTCCGAA' AACTCCGAA'	rgccg-tggt	G-TAMA-GCGT	GGCA M.kansasii GGAA M.smegmatis
3486	6 CAGCCA	AACTCCGAA'	tgccgGtAag	GCCAAGAGIIGC	GGA M.smegmatis
3.0					
		1170	1180	1190	1200
1.40	A TOTGG	DAAGGATGT	GTAGTCGCA	A-GACAACCA	GGAGG M.avium
142	5 AGTGG	AAAAGGATG	GTAGTCGCA	BA-GACAACCA	GGAGG M.paratuberc. GGAGG M.tuberculosis
212	2 AGTGG	GAAAGGATG:	rgdagtcgca	NA-GACAACCA	GGAGG M.tuberculosis GGAGG M.phlei
151	L9 AGTGG	AAAAGGATG:	recae andeed	Th - CACAACCA	GGAGG M.leprae
144	41 AGTGG	AAAAGGATG	1000000	an chennech	GGAGG M.gastri
12:	15 AGTGG	GAAAGGATG	TGCAGTCGCA	GA-GACAACCA	AGGAGG M.kansasii AGGAGG M.smegmatis
3 E	06 AGIGG 06 AGIGG	AAAAGGATG	TGAAGTCGCA	GAAGAAACCA	AGGAGG M.smegmatis
30			_ -		

	1250	126			1280	
1504 2201 1598	CTCACTGGTCA CTCACTGGTCA CTCACTGGTCA CTCACTGGTCA	AGTGATTAT AGTGATTGT AGTGATTGT AGTGATTGT AGTGATTGT	GCGCCGA1 GCGCCGA1 GCGCCGA1 GCGCCGA1	TATGTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GG M GGG M GGG M GGG M	.tuberculosis .phlei .leprae .gastri .kansasii
	129		00	1310	1320	
1544 2241	CTCAAGCACAC CTCAAGCACAC CTCAAGCACAC CTCAAGCACAC	CGCCGAAG CCGCCGAAG CCGCCGAAG CCGCCGAAG	CCGCGGCA CCGCGGCA CCGCGGCA CCGCGACA	CATGCAGCTT -ATCAGCTT CATTCAGCTT CATTCAGCTTACCGC	GT- I TTG I CTA I A	M.tuberculosis M.phlei
		20 1	340	1350	136	0
1583 1583 2284 167 160 136 131	O FGGTGGTGT 6 TGGCTGGTGT 0 GGGTGGATGT 7 AGGTFT	GGGTAGGGGGGGGGTAGGGGGGTAGGGGGTAGGGGGTAGGGGGG	EAGCGTCC EAGCGTCC EAGCGTCC EAGCGTTCC EAGCGTTCC	CCCATTCAGC CCCATTCAGC CTCATTCAGC TGCATTCAGC CTCATTCAGC	GAAG GAAG GAAG GAAG	M.tuberculosis M.phlei M.leprae

Figure 4F

-	1370	1380	1390	1400
1623 C 2319 C 1716 C 1640 C 1402 C	CACCGGGTGACCGG CCCCGATGATICGG CTCCGGGTACCGG CCGCCGGTGACCGG	TEGTEGREGE TEGTEGREGE TEGTEGREGE TEGTEGREGE TEGTEGREGE	TGGGGGAGTG TGGGGGAGTG TGGGGAAGTG TGGGGGAGTG	AGAAT M.tuberculosis
			. .	
				
	1530	1540	1550	1560
1781 2479 1875 1800 1562	CGATGGACAACGGG CGATGGACAACGGG CGATGGACAACGGG CGATGGACAACGGG	TTGATATTCC TTGATATTCC TTGATATTCC TTGATATTCC	CGTACCCGTG CGTACCCGTG CGTACCCGTG	TATGGG M.avium TATGGG M.paratuberc. TGTGGG M.tuberculosis TATGAG M.phlei TGTGTG M.leprae TGTGGG M.gastri TGTGGG M.kansasii TATGTG M.smegmatis
	1570	1580	1590	1600
1821 2519 1915	CGTCCCTGATGAA' CGGCCGTGATGAA CGGCCGTGATGAA CGGCCGTGATGAA	TCA-GCGGTAC TCA-GCGGTAC TCTCATTCTGC TCA-GCGGTAC TCA-GCGGTAC	TTAACCACCCCCTTAACCACCCCCCCCCCCCCCCCCCC	AAAACCG M.avium AAAACCG M.paratuberc. AAAACCG M.tuberculosis AAAACCM M.phlei AAAACCG M.leprae AAAACCG M.gastri AAAACCG M.kansasii

Figure 4G

					
	1610	1620	1630	1640	
			C-GTGGCGAT	T-CGG M.avium	
				CILCO II. CODOLOGICA	
		*CCCTTCCCCCCC.	リリーしゃ ししゃしっかいしんごし	M-MG M. 9 CD CD	
1584	GAT-CGALICAC-TC		-derecent	TGGTGG M.smegmatis	
4035	ACCGIGACCGCAC	1100000			
				1.000	
	1650	1660	1670	1680	
1006	CCCTCCCTCCCACC	TTCGCTGGTA	TAGTCAAGO	AATGGG M.avium	
1896	CCCTCCCTCGGAC	CTTCGCTGGTA	STAGTCAAGC	AATGGG M.paratuberc.	
		へんていたかんにはなかない	TTAGTCAAGO	GAIGGG M. PHICE	
16//	GGCTGCGTGGACC	СТТСССТССТА	GTAGTCAAGC	GATGGG M.kansasii	
1620	CCCTCCTTCCGAC	CTTCGTTGGTA	GTAGTCAAGC	GATGGG M.smegmatis	
4071	GGCIGCMIGOONO	01100		_	
			1710	1720	
	1690	1700	1710		
1026	-GTGACGCAGGAA	GGCAGCCGTAC	CAGTCAGTGG	TAATA- M.avium	
					3
		reemmaccciailat	こことにいいい	JIARIA IIIPIIII	
		. ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	"("A) - "(A) - (t	TIARIA II. GUDUE	
/1111	-GTGACGCAGGA	AGGMAGCCGTAG	CCGGTCAGTG	STAATA- M.smegmatis	
4111	[Glorocovico:1		_		
			1750	1760	
	1730	1740	1750		
197	4 -CTGGGGCAAGC	CCGTAGAGA	GCGATAGGCA	AATCCGT M.avium AATCCGT M.paratuberc.	
197	4 -CTGGGGCAAGC	CCGTAGAGA	GCGATAGGCA	AATCCGT M.paratuberc.	~
267	2 -CTGGGGCAAGC	CGGTAGGGAGA	GCGATAGGCA	AATCCGT M.tuberculosi	. >
100	5 -CTGGAGCAAGC	CCGTAGGGAGA	GCGATAGGCA	AATCCGT M.leprae	
414	9 -cBggBgffaagc	CHGTAGGGAGI	CAGATAGGIA	AATCCGT M.smegmatis	
7.7.7	> 0/0/0 0 [0] - [0] -				

Figure 4H

		1810	1820	1830	1840
0051	CC - NATT	CGTGATCC	TCTGCTGCCA	AGAAAAGCC	TCTA- M.avium
2051	CG ANTE	CGGTGATCC'	TCTGCTGCCA	AGAAAAGCC'	TCTA- M.paratuberc.
2051	CG-AAII	CCCTGATCC'	TCTGCTGCCF	AGAAAAGCC'	TCTA- M.tuberculosis
2751	CG-AATT	CGGIGAICC CCCCCATCC	TATECTETICS	AGAAAAGCC	TCTA- M.phlei TCTA- M.leprae
2141	CG-AATT		тетестесси	AGAAAAGCC	TCTA- M.leprae TCTA- M.gastri
2074	CG-AATT	CGGTAAGCC	TCTGCTGCC!	AGAAAAGCC	TCTA- M.gastri
1777	CG-AATT	CGGTGATCC		BAGAAAAGCC	TCTA- M.smegmatis
4228	CG-AATT	CGGTGATCC	.THIGGIOCOL	3 , 10	
		1050	1860	1870	1880
		1850			CRCCT M avium
2089	GCGAGCA	CATACACGG	CCCGTACCC	CAAACCAACA	CAGGT M.avium
2089	GCGAGCA	CATACACTG	CCCGTACCC		CAGGT M.paratuberc.
2789	GCGAGCA	CADACACGG	CCCGTACCC	CAAACCGACA	CAGGT M.tuberculosis
2179	GCAAGC	CATACACGG	CCCGTACCC	CAAACCAACA	CAGGT M.phlei CAGGT M.leprae
2112	GCGAGCE	MACATGCGG	CCCGTACCC	CAAACCGACA	ACAGGT M.leprae
1072	GCGAGCA	CACACACGO	CCCGTACCC	CAAACCGACA	ACAGG M.gastri ACAGGT M.kansasii
1015	GCGAGC	CACACACGO	CCCGTACCC	CAAACCGACA	ACAGGT M.kansasii
1010	cccaed?	CATACACGO	CCCGTACCC	CAAACCAACA	ACAGGT M.smegmatis
4200	GCGYOD!	.0.12110			
			,		
		1970	1980	1990	2000
				CCTTCCGGT	GGGAGC M.avium
2208	B AGGGGG	<u>CCCGGAATA</u>	CCGTGAACAC	CCIIGCGGI	GGGAGC M.paratuberc.
2208	B AGGGGG	CCCGGAATA	CCGTGAACA	JCC11GCGG1	GGGAGC M.paratuberc.
2298	8 AGGGGG	ACCCACGTA	CCGTGAGGG		GGGAGC M.phlei
223	1 AGGGGG	GCCGGAATA	ДCGTGAACA	CCCLLecee1	GGGAGC M.leprae M.gastri
191	0	_			Migabor-
193	4 AGGGGG	ACCGGAATA	CCGTGAACA	CCCTTGCGGI	GGGAGC M.kansasii
438	5 AGGGGG	PACCEAGATE	GCGTGTAAG	CCITTACGGE	CCCAAGC M.smegmatis
450					
			_		
			2020	2030	2040
		2010	2020		m cmmmb M avium
22.4	8 GGGAT	TCGGCCGCA	GAAACCAGT	GGTAGCGAC	T-GTTTA M.avium T-GTTTA M.paratuberc.
224	IR GGGAT	TCGGCCGCA	GAAACCAGT	GGTAGCGAC	T-GTTTA M.paratuberc.
294	18 GGGAT	OCCEPTICGCA	GAAACCAGT	FAGGAGCGAC	T-GTTTA M.tuberculosis T-GTTTA M.phlei
233	se cec <u>ec</u>	TEGETECA	Caaaccagt(SAGGAGCGAC	T-GTTTA M.phlei
23	71 GGGAT	CCGTCGCA	GAGACCAGT	SAGAAGCGAC	
10.	,, GGGA1	□			M.gastri
19.	14 GGGDU	TCGGMCGCA	GAAACCAGT	GAGAAGCGAC	TTGTTTA M.kansasii CT-GTTTA M.smegmatis
19	74 GGGAI		HAAACCAGT	GAGAAGCGAC	CT-GTTTA M.smegmatis
44:	72 GTG 4F	115000 0000			

Figure 4I

					———	
	213		.170	2150	2160	
2367 2367 3067 2457 2390 1910 2094 4544	CCGTTAACCC CCGTTAACCC CCGTTAACCC	STAAGG SGAAGG TTTCGGGG GAAAGG	GTGAAGCGG GTGAAGCGG GTGAAGCGG GTGAAGCGG	AGAATTTAAG AGAATTTAAG	CCC M. CCC M. CCC M. CCC M. CCC M.	tuberculosis phlei leprae gastri kansasii
			-	-		
		50	2260	2270	2280	
2485 3185 2577 2508	GTAACGACT' GTAACGACT' GTAACGACT'	rcccaact rctcaact rctcaact rctcaact	GTCTCAACC. GTCTCAACC. GTCTCAACC	ATAGACTCGG ATAGACTCGG ATAGACTCGG	CGAA N CGAA N CGAA N	M.tuberculosis M.phlei M.leprae M.gastri
	2	370	2380	2390	2400	
260 260 330 269 262 191 233	5 GTTCGGTA 7 G@TCGATA 28 GTTCGGT@ 10	CGGTTTGT CGGTTTGT CGGTTTGT CGGTTTGT	GTAGGATAG GTAGGATAG GTAGGATAG GTAGGATAG	GTGGGAGACT GTGGGAGACT GTGGGAGACT	GTGAA GTGAA GTGAA	M.tuberculosis M.phlei

Figure 4J

				
	2410			440
393 AT 2645 GC 3345 AC 284 AC 2737 GC 2668 AC	ACAGACGCCAGTT CTCGACGCCAGTT CTCGACGCCAGTT TCGGACGCCAGTT TTCGACGCCAGTT	retgregaeree Geedgeaetee Geedgeaetee Geetgeaetee Eggetgeaete	TTGTTGAAATA(TTGTTGAAATA(TTGTTGAAATA(TTGTTGAAATA TTGTTGAAATA	CC M.paratuberc. CC M.tuberculosis CC M.bovis CC M.phlei CC M.leprae M.gastri
	2450	2460	2310	2480
433 A 2685 A 3385 A 324 A 2777 A 2708 A	CTCTGATCGTATT CTCTGATCGTATT CTCTGATCGTATT ACTCTGATCGTATT ACTCTGATCGTATT ACTCTGAT	GGACACCTAACG GGACACCTAACG GGGCATCTAACC GGGCCTCTAACC GAACATCTAACC	rcgaacct-t/ rcgaacctga rcgaacctga rcggaccftgg rcgaaccgtat	ATC M.paratuberc. ATC M.tuberculosis ATC M.bovis ATC M.phlei
-	2690	2700	2710	2720
2924 3625 3017 2948 1910	GGTGTCACTCAAC GGTGTCACTCAAC GGTGTCGCTCAAC GGTGTCGCTCAAC	CGGATAAAAGGTA CGGATAAAAGGTA CGGATAAAAGGTA	ACCCGGGGAT ACCCCGGGGAT ACCCCGGGGAT	AACAG M.avium AACAG M.paratuberc. AACAG M.tuberculosis AACAG M.phlei AACAG M.leprae M.gastri AACAG M.kansasii AACAG M.smegmatis
	2730	2740	2750	2760
2964 3665 3057 2988 1910	GCTGATCTTCCC GCTGATCTTCCC GCTGATCTTCCC GCTGATCTTCCC	CAAGAGTCCATA CAAGAGTCCATA CAAGAGTCCATA CAAGAGTCCATA	TCGACGGGAT(TCGACGGGAT(TCGACGGGAT(GGTTTG M.avium GGTTTG M.paratuberc. GGTTTG M.tuberculosis GGTTTG M.phlei GGTTTG M.leprae M.gastri GGTTTG M.kansasii GGTTTG M.smegmatis

Figure 4K

-	277		2780	2790	2800)
_	211			TO T	CCB	M avium
3004	CACCTCGAT	STCGGCT	CGTCGCATCC	TGGGGCTGGA	GCA	M paratuberc.
3004	CACCTCGAT	STCGGCT	CGTCGCATCC	TGGGGCTGGA	CCR	M.paratuberc.
3705	GCACCTCGAT(STCGGCT	CGTCGCATCC	TGGGGCIGGA	CCA	M.tuberculosis
3097 (GCACCTCGAT(GTCGGCT	CGTCGCATCC	TGGGGCTGGA	CCA	M leprae
3028	GCACCTCGAT(GTCGGCT	CGTCGCATCC	TGGGGCTGAA	CA	M.gastri
1910				rmcccccrccr	\CCA	
2732	GCACCTCGAT	GTCGGCI	CGTCGCATCC	TGGGGCTGGF		M.kansasii M.smeqmatis
5182	GCACCTCGAT	GTCGGCI	CGTCGCATC	TGGGGCTGGF	KUCA	M.smegmatis
-						
	281	.0	2820	2830	284	0
		~~~~	memmedece-	-ATTAAAGCGG	CAC	M.avium
3044	GGTCCCAAGG	GTTGGGC	TGTTCGCCC CMCMMCGCCCC	-ATTABAGCG0	CAC	M.tuberculosis
3745	GGTCCCAAGG	GTTGGGC		-ATTAAAGCG(	CAC	M.phlei
3137	GGTCCCAAGG	GTTGGGC	7161106000	-ATTAAAGCG(	GCAC	M.leprae
1910				- ATTABAGCG(	GCAC	M.kansasii
2772	GGTCCCAAGG	G.L.T.G.G.C.	CTGTTCGCCC	HATTABAGCG	GCAC	M.smegmatis
5222	GGTCCCAAGG	SUTTERS		Dr. 11. 2 10 11		-
				- <b>-</b>		
			. *			
	•			0070	2001	<b>1</b>
	305	50	3060	3070	3080	
2283			an accommon o	TACCATARG	ccc	M.avium
	CAAGATCAGG	TTT-CT	CACCOTTTTAC	AGGATAAGG	ccc sccc	M.avium M.intracellulare
638	CAAGATCAGG CAAGATCAGG	TTT-CTC	CACCOTTTTAC	GAGGATAAGG	ccc	M.avium M.intracellulare M.paratuberc.
638	CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CTC	CACCOTTTTAC CACCOTTTTAC	GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG	3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis
638 3283 3984	CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CTC; TTT-CTC; TTT-CTC;	CACCOTTTTAC CACCCTTTTAC CACCCACTTG	SAGGATAAGG SAGGGATAAGG SAGGGATAAGG STGGGATAAGG	3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis
638 3283 3984	CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CTC; TTT-CTC; TTT-CTC;	CACCOTTTTAC CACCCTTTTAC CACCCACTTG	SAGGATAAGG SAGGGATAAGG SAGGGATAAGG STGGGATAAGG	3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei
638 3283 3984 570 3376	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CTC; TTT-CTC; TTT-CTC;	CACCOTTTTAC CACCCTTTTAC CACCCACTTG	GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG	3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae
638 3283 3984 570 3376 3307	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	7TT-CTC; 7TTT-CTC; 7TTT-CTC; 7TTT-CTC; 5TTT-CTC;	CACCOTTTTAC CACCCTTTTAC CACCCACTTGC CACCCACTTGC CACCCACTTGC	SASGGATAAGG SAGGGATAAGG SAGGGATAAGG STGGGATAAGG GTGGGATAAGG GAGGGATAAGG	3000 3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri
638 3283 3984 570 3376 3307 1910	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT(	CACCOTTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC	EABGGATAAGG EAGGGATAAGG EAGGGATAAGG ETGGGATAAGG GTGGGATAAGG	3000 3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii
638 3283 3984 570 3376 3307 1910	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT(	CACCOTTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC	EABGGATAAGG EAGGGATAAGG EAGGGATAAGG ETGGGATAAGG GTGGGATAAGG	3000 3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii
638 3283 3984 570 3376 3307 1910	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT(	CACCOTTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC	EABGGATAAGG EAGGGATAAGG EAGGGATAAGG ETGGGATAAGG GTGGGATAAGG	3000 3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri
638 3283 3984 570 3376 3307 1910	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT( TTT-CT(	CACCOTTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC	EABGGATAAGG EAGGGATAAGG EAGGGATAAGG ETGGGATAAGG GTGGGATAAGG	3000 3000 3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii M.smegmatis
638 3283 3984 570 3376 3307 1910	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC	CACCOTTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC	EABGGATAAGG EAGGGATAAGG EAGGGATAAGG ETGGGATAAGG GTGGGATAAGG	3000 3000 3000 3000 3000	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii M.smegmatis
638 3283 3984 570 3376 3307 1910 3011 5462	CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG CAAGATCAGG	TTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC	CACCOTTTAC CACCCACTTG CACCACTTG CACCCACTTG CACCACTTG CACCCACTTG CACCACTTG CACCACTTG CACCACTTG CACCACTTG CACCACTTG CACCACTTC CACCACTT	EAEGGATAAGG EAGGGATAAGG ETGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG	GCCC GCCC GCCC GCCC GCCC GCCC	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii M.smegmatis
638 3283 3984 570 3376 3307 1910 3011 5462	CAAGATCAGG	TTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC	CACCOTTTAC CACCCACTTG CACCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCACTTG CAC	EAEGGATAAGG EAGGGATAAGG ETGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG	GCCC GCCC GCCC GCCC GCCC GCCC AGCT	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii M.smegmatis
638 3283 3984 570 3376 3307 1910 3011 5462 3322 677	CAAGATCAGG CCAAGATCAGG CCAAGATCAGG	TTT-CTC TTT-CTC TTT-CTC TTT-CTC TTT-CTC TTT-CTC TTT-CTC TTT-CTC TTT-CTC	CACCOTTTTAC CACCCTTTTAC CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCTGTAG  3100 ATTGATAGGC	EAEGGATAAGG EAGGGATAAGG ETGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG	GCCC GCCC GCCC GCCC GCCC GCCC	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii M.smegmatis
638 3283 3984 570 3376 3307 1910 3011 5462 3322 677	CAAGATCAGG CCAAGATCAGG CCAGATCAGG CCAGCAGA	TTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTT-CTC	CACCOTTTTAC CACCCACTTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC CACCCACTTAC  CACCCACTTAC  3100  ATTGATAGGC ATTGATAGGC	EASGGATAAGG EAGGGATAAGG ETGGGATAAGG GTGGGATAAGG GTGGGATAAGG GTGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG	GCCC GCCC GCCC GCCC GCCC GCCC AGCT AGCT	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii M.smegmatis  20 M.avium M.intracellulare M.paratuberc. M.tuberculosis
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638 3283 3984 570 3376 3307 1910 3011 5462 3322 677 3322 4023 609	CAAGATCAGG CCAAGATCAGG CCAGATCAGG CCAGCAGA	TTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTTT-CTC TTT-CTC TTT-CT	CACCOTTTTAC CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCACTTG CACCCTGTAG  3100 ATTGATAGGC CATTGATAGGC CATTGATAGGC CATTGATAGGC	EASGEATAAGG EAGGEATAAGG ETGGGATAAGG GTGGGATAAGG GTGGGATAAGG GTGGGATAAGG GAGGGATAAGG GAGGGATAAGG GAGGGATAAGG CAGACCTGGA CCAGACCTGGA	GCCC GCCC GCCC GCCC GCCC GCCC AGCT AGCT	M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri M.kansasii M.smegmatis  O M.avium M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei
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Figure 4L

	130	140	150	160	
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59					
107					
70			'CCAC'I''I'C#G	JUATAA M. CUDELCULU-	sis
70			162 (- 0.1 - 11 - 12 - 12 1	TITALAA MADOVED	
209					
120	GAGTAACACGTGGG	HAATCIGCCCI	CCVCPCC=G	GGATAA M.kansasii	
69					
70	GAGTAACACGTGGG	CAATCTGCCCI	CACAGO G	GGATAA M.gordonae	
104	GAGTAACACGTGGG	ATCTGCCC1	rccncmrc-6	GGATAA M.marinum	
64	GAGTAACACGTGGG	CGATCTGCCC	IGCACTIC O	00/11/21	
		-			
		460	470	480	
	450	460			
424	AAACCTCTTTCAC	CATCGACGAAG	GTCCGGG <u>TT</u>	TTCTCGG M.avium	ulare
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528		~~ ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	CTCCGGGGTT	CITCICGG MIDOVID	
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381	ABACCTCTTTCAC	CATCGACGAA	GTECGGGTT	TTCTCGG M.marinum	
201	AAACCICIIIO		_		
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	490		T GGGGGGT	CTACGTG M.tubercul	osis
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568					
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421	ATTCACCGTAGGT	GGAGAAGAAG	CACCGGCCA	ACTACGTG M.marinum	
421	WIIGHOOG INGO	= =			•

# Figure 5A

1130 1140 1150 1160  1104 TCTCATGTTGCCAGGGGTANTGC GGGGACTGTGAGAG M. avium 1056 TCTCATGTTGCCAGGGGTANTGCGGGGACTGTGAGAG M. intracellulare 1068 TCTCATGTTGCCAGCGGGTANTGCAGGGGACTGTGAGAG M. paratuberc. 1069 TCTCATGTTGCCAGCGGGTANTGCTGGGGGACTGGTGAGAG M. paratuberc. 1069 TCTCATGTTGCCAGCAGGTANTGCTGGGGGACTGGTGAGAG M. tuberculosis 1208 TCTCATGTTGCCAGCAGGTANTGTGGGGGACTGGTGAGAG M. tuberculosis 1219 TCTCATGTTGCCAGCAGGTANTGTGGGGACTCGTGAGAG M. bovis 1119 TCTCATGTTGCCAGCAGGTANTGTGGGGACTCGTGAGAG M. leprae 1066 TCTCATGTTGCCAGCGGGTATGCGGGGACTCGTGAGAG M. gartri 1070 TCTCATGTTGCCAGCGGGTANTGCCGGGACTCGTGAGAG M. gardonae 1081 TCTCATGTTGCCAGCGGGTANTGCCGGGGACTCGTGAGAG M. gardonae 1082 TCTCATGTTGCCAGCGGGTANTGCCGGGGACTCGTGAGAG M. gardonae 1083 TCTCATGTTGCCAGCGGGTANTGCCGGGGACTCGTGAGAG M. gardonae 1084 CGAATCCTTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. marinum 1290 1300 1310 1320  1264 CGAATCCTTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. paratuberc. 1258 CGAATCCTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. bardaceum 1292 CGAATCCTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. bardaceum 1293 CGAATCCTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. bardaceum 1294 CGAATCCTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. leprae 1205 CGAATCCTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. kansasii 1207 CGAATCCTTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. kansasii 1207 CGAATCCTTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. gastri 1208 CGAATCCTTTTANAGCCGGTCTCAGTTCGGATTGGGGTCT M. gastri 1209 CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT M. gastri 1210 CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT M. gastri 1221 CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT M. gastri 1222 CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT M. gastri 1223 CGAATCCTTTTAAGCCGGTCTCAGTTCGGATTGGGGTCT M. gastri 1224 CGAATCGACCCTTGAAGTCGGAGTCGCTAGTAATCGCA M. paratuberc. 1225 CGAATCCTTTTAAGCCGTCTTAGTTCGGATTGGATTAGCCA M. paratuberc. 1226 CGAATCGACCCTTGAAGTTGGAGTCGCTAGTAATCGCA M. paratuberc. 1227 CGAATCGACCCTTGAAGTCGGAGTCGCTAGTAATCGCA M. tuberculosis 1407 CGAACTCGACCCTTGAAGTCGGAGTCGCTAGTAATCGCA M. hovis 1407 CGAACTCGACCCTTGAAGTCGGAGTCGCTAGTAATCGCA M. herculosis 1407 CGAACTCGACCCCTTGAAGTCGGAGTCGCTAGTAATCGCA M					<del></del>
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1330 1340 1350  1304 GCAACTCGACCCCAFGAAGTCGGAGTCGCTAGTAATCGCA M.avium  1256 GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA M.intracellulare  1298 GCAACTAGACCCATGAAGTCGGAGTCGCTAGTAATCGCA M.paratuberc.  1264 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.scrofulaceum  1268 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.bovis  1407 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.leprae  1319 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.kansasii  1266 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.gastri  1267 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.gastri					
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1319 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.kansasii 1266 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.gastri 1267 GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA M.gordonae	1268	GCAACICGACCCC	CTCAAGTCGG	AGTCGCTAGT	AATCGCA M.bovis
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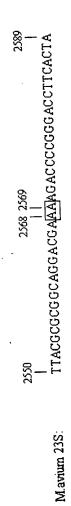


Figure 6

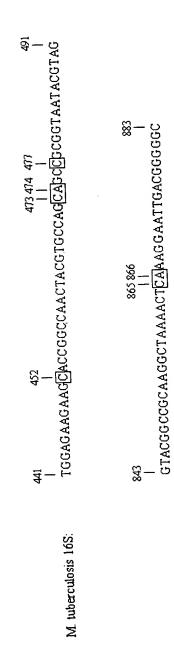


Figure 7